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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:49:28 ; Search time 803.766 Seconds
(without alignments)
9466.331 Million cell updates/sec

Title: US-09-807-933B-4
Perfect score: 1101
Sequence: 1 atgaagtttattactattac.....caggttgttcaagaaaataa 1101

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7796847 seqs, 3455365420 residues

Total number of hits satisfying chosen parameters: 15593694

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1101	100.0	1101	6	US-09-807-933B-4	Sequence 4, Appli
	2	763	69.3	1017	6	US-09-807-933B-2	Sequence 2, Appli
	3	763	69.3	1017	8	US-10-380-420-1	Sequence 1, Appli
	4	519	47.1	1083	6	US-09-807-933B-6	Sequence 6, Appli
	5	421.2	38.3	1043	6	US-09-807-933B-13	Sequence 13, Appl
	6	390.2	35.4	1164	6	US-09-807-933B-10	Sequence 10, Appl
	7	367.4	33.4	1017	6	US-09-807-933B-8	Sequence 8, Appli
	8	289.6	26.3	1041	6	US-09-807-933B-12	Sequence 12, Appl
	9	109.8	10.0	890	8	US-10-369-493-27891	Sequence 27891, A
	10	96.8	8.8	423	8	US-10-205-189A-241	Sequence 241, App
	11	94.6	8.6	627	8	US-10-205-189A-233	Sequence 233, App
	12	94	8.5	428	8	US-10-205-189A-244	Sequence 244, App
	13	92.4	8.4	416	8	US-10-205-189A-256	Sequence 256, App
	14	90.8	8.2	417	8	US-10-205-189A-278	Sequence 278, App
	15	89.8	8.2	1257	8	US-10-380-420-5	Sequence 5, Appli
	16	89.8	8.2	1257	8	US-10-416-328-7	Sequence 7, Appli
	17	89.4	8.1	5046	6	US-09-548-938A-5	Sequence 5, Appli
	18	88	8.0	390	8	US-10-205-189A-255	Sequence 255, App
c	19	87	7.9	154	6	US-09-807-933B-94	Sequence 94, Appl
c	20	83.4	7.6	118	6	US-09-807-933B-92	Sequence 92, Appl
	21	83.4	7.6	298	8	US-10-205-189A-294	Sequence 294, App
	22	82	7.4	154	6	US-09-807-933B-93	Sequence 93, Appl
	23	80.6	7.3	449	8	US-10-205-189A-234	Sequence 234, App
c	24	80	7.3	120	6	US-09-807-933B-91	Sequence 91, Appl
c	25	79.6	7.2	160	6	US-09-807-933B-90	Sequence 90, Appl
	26	79.6	7.2	450	8	US-10-205-189A-258	Sequence 258, App
	27	77.4	7.0	448	8	US-10-205-189A-236	Sequence 236, App
	28	76.8	7.0	361	8	US-10-205-189A-268	Sequence 268, App
	29	75.2	6.8	453	8	US-10-205-189A-235	Sequence 235, App
	30	74	6.7	117	6	US-09-807-933B-95	Sequence 95, Appl
	31	73.8	6.7	441	8	US-10-205-189A-238	Sequence 238, App
	32	73.2	6.6	368	8	US-10-205-189A-261	Sequence 261, App
	33	73.2	6.6	450	8	US-10-205-189A-253	Sequence 253, App
	34	72.8	6.6	420	8	US-10-205-189A-240	Sequence 240, App
	35	72.4	6.6	132	6	US-09-807-933B-86	Sequence 86, Appl
	36	71.8	6.5	367	8	US-10-205-189A-272	Sequence 272, App
	37	71.8	6.5	392	8	US-10-205-189A-264	Sequence 264, App
	38	71.8	6.5	405	8	US-10-205-189A-237	Sequence 237, App
	39	71.2	6.5	424	8	US-10-205-189A-265	Sequence 265, App
	40	71.2	6.5	434	8	US-10-205-189A-270	Sequence 270, App
	41	69.6	6.3	273	8	US-10-205-189A-311	Sequence 311, App
	42	69.6	6.3	399	8	US-10-205-189A-263	Sequence 263, App
	43	69.6	6.3	404	8	US-10-205-189A-260	Sequence 260, App
	44	69.6	6.3	412	8	US-10-205-189A-269	Sequence 269, App
	45	69.6	6.3	413	8	US-10-205-189A-262	Sequence 262, App

ALIGNMENTS

RESULT 1
US-09-807-933B-4
; Sequence 4, Application US/09807933B
; GENERAL INFORMATION:
; APPLICANT: MEIJI SEIKA KAISHA, LTD.
; TITLE OF INVENTION: Endoglucanase and cellulase composition containing the
; TITLE OF INVENTION: same
; FILE REFERENCE: 121659PX
; CURRENT APPLICATION NUMBER: US/09/807,933B
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: JP302387/1998
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1101
; TYPE: DNA
; ORGANISM: Rhizopus oryzae CP96001
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(69)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (70)..(1101)
US-09-807-933B-4

Query Match 100.0%; Score 1101; DB 6; Length 1101;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAAGTTTATTACTATTACCTCTTCCGCTCTCTTGGCTCTCGCCCTTGGTACTGAAATG 60
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Db          1 ATGAAGTTTATTACTATTACCTCTTCCGCTCTCTTGGCTCTCGCCCTTGGTACTGAAATG 60

Qy         61 GCCTCTGCTGCTAAATGTAGCAAGCTGTATGGTCAATGTGGTGGTAAGGACTGGAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCTCTGCTGCTAAATGTAGCAAGCTGTATGGTCAATGTGGTGGTAAGGACTGGAATGGC 120

Qy        121 CCTACTTGTTGCGAATCTGGATCCACCTGTAAAGTAAGCAACGATTACTACTCTCAATGT 180
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Db        121 CCTACTTGTTGCGAATCTGGATCCACCTGTAAAGTAAGCAACGATTACTACTCTCAATGT 180

Qy        181 CTTGCCCCTGAAAGCAACGGCAATAAGTCTTCTGAATGTAGCAAGTTGTATGGTCAATGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTTGCCCCTGAAAGCAACGGCAATAAGTCTTCTGAATGTAGCAAGTTGTATGGTCAATGT 240
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Qy        241 GGTGGTAAGGACTGGAATGGCCCTACTTGTTGCGAATCTGGATCCACCTGTAAAGTAAGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGTGGTAAGGACTGGAATGGCCCTACTTGTTGCGAATCTGGATCCACCTGTAAAGTAAGC 300

Qy        301 AACGATTACTACTCTCAATGTCTTGCCCCTGAAAGCAATGGCAATAAAACTTCTGAAAGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AACGATTACTACTCTCAATGTCTTGCCCCTGAAAGCAATGGCAATAAAACTTCTGAAAGC 360

Qy        361 GCTCATAAAACGACTACTACCACTGCTCCCGCTAAGGAAATTACAACTACTGCCAAAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCTCATAAAACGACTACTACCACTGCTCCCGCTAAGGAAATTACAACTACTGCCAAAGCT 420

Qy        421 TCAAACTCTTCTAACTCTAGCGGCAAATACTCCATTGTCTCTGGTGGTGCCTCTGGTAAC 480
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Db        421 TCAAACTCTTCTAACTCTAGCGGCAAATACTCCATTGTCTCTGGTGGTGCCTCTGGTAAC 480

Qy        481 GGTGTCACTACTCGTTATTGGGATTGCTGTAAGGCCTCCTGTAGCTGGCCCGGTAAGGCC 540
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Db        481 GGTGTCACTACTCGTTATTGGGATTGCTGTAAGGCCTCCTGTAGCTGGCCCGGTAAGGCC 540

Qy        541 AATGTCAGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCACTGCCCTTAGTGACAGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AATGTCAGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCACTGCCCTTAGTGACAGC 600

Qy        601 AATGTCCAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTAACGACAACCAGCCTTGG 660
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Db        601 AATGTCCAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTAACGACAACCAGCCTTGG 660

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Db        781 AAGATGGTTATCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCTACTGGTGCTCAC 840

Qy        841 TTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATGGTTGCTCCAAGCAATGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATGGTTGCTCCAAGCAATGG 900

Qy        901 GGTGCTCCCAATGACGGTTGGGGCTCGAGATACGGTGGTATTTCTTCTGCATCTGACTGC 960
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Db        901 GGTGCTCCCAATGACGGTTGGGGCTCGAGATACGGTGGTATTTCTTCTGCATCTGACTGC 960

Qy        961 TCTAGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAAC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1021 GCTGATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCCAAGGAAATCACCGCCAAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCTGATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCCAAGGAAATCACCGCCAAG 1080

Qy       1081 ACAGGTTGTTCAAGAAAATAA 1101
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RESULT 2
US-09-807-933B-2
; Sequence 2, Application US/09807933B
; GENERAL INFORMATION:
; APPLICANT: MEIJI SEIKA KAISHA, LTD.
; TITLE OF INVENTION: Endoglucanase and cellulase composition containing the
; TITLE OF INVENTION: same
; FILE REFERENCE: 121659PX
; CURRENT APPLICATION NUMBER: US/09/807,933B
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: JP302387/1998
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Rhizopus oryzae CP96001
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(69)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (70)..(1017)
US-09-807-933B-2

Query Match 69.3%; Score 763; DB 6; Length 1017;
Best Local Similarity 90.3%; Pred. No. 1.7e-219;
Matches 858; Conservative 0; Mismatches 35; Indels 57; Gaps 2;

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Db         68 CTGCTGAATGTAGCAAATTGTATGGTCAATGTGGTGGTAAGAACTGGAATGGCCCTACTT 127

Qy        269 GTTGCGAATCTGGATCCACCTGTAAAGTAAGCAACGATTACTACTCTCAATGTCTTGCCC 328
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Qy        376 -------------------------------ACTACCACTGCTCCCGCTAAGGAAATTA 403
                                            |||||||||||||| |||||| | | ||
Db        248 ACAAGAAGACTACTACCGCTGCTCATAAAAAGACTACCACTGCTCCTGCTAAGAAGACTA 307

Qy        404 CAACTACTGCCAAAGCTTCAAACTCTTCTAACTCT------------AGCGGCAAATACT 451
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Db        308 CAACTGTTGCCAAAGCTTCCACCCCTTCTAACTCTAGCTCTAGCTCCAGCGGCAAATATT 367

Qy        452 CCATTGTCTCTGGTGGTGCCTCTGGTAACGGTGTCACTACTCGTTATTGGGATTGCTGTA 511
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Db        368 CCGCTGTCTCTGGTGGTGCCTCTGGTAACGGTGTCACTACTCGTTATTGGGATTGCTGTA 427

Qy        512 AGGCCTCCTGTAGCTGGCCCGGTAAGGCCAATGTCAGTTCTCCTGTCAAGTCCTGTAACA 571
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Db        428 AGGCCTCCTGTAGCTGGCCCGGTAAGGCCAATGTCAGTTCTCCTGTCAAGTCCTGTAACA 487

Qy        572 AAGATGGTGTCACTGCCCTTAGTGACAGCAATGTCCAAAGTGGCTGTAACGGTGGTAACA 631
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Db        488 AAGATGGTGTCACTGCCCTTAGTGACAGCAATGCCCAAAGTGGCTGTAACGGTGGTAACA 547

Qy        632 GTTACATGTGTAACGACAACCAGCCTTGGGCTGTAAACGATAATCTTGCCTATGGTTTCG 691
              |||||||||||||||||||| |||||||||||||||| || ||||||||||||||||||
Db        548 GTTACATGTGTAACGACAACCAACCTTGGGCTGTAAACGACAACCTTGCCTATGGTTTCG 607

Qy        692 CTGCTGCTGCCATCAGTGGTGGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTA 751
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Db        608 CTGCTGCTGCCATCAGTGGTGGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTA 667

Qy        752 CTTTCACTTCTACCTCTGTTGCTGGTAAGAAGATGGTTATCCAAGTCACTAACACTGGTG 811
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CTTTCACTTCTACCTCTGTTGCTGGTAAGAAGATGGTTGTCCAAGTCACTAACACTGGTG 727

Qy        812 GTGATCTTGGCTCCTCTACTGGTGCTCACTTTGACTTGCAAATGCCCGGTGGTGGTGTTG 871
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 GTGATCTTGGCTCCTCTACTGGTGCTCACTTTGACTTGCAAATGCCCGGTGGTGGTGTTG 787

Qy        872 GTATTTTCAATGGTTGCTCCAAGCAATGGGGTGCTCCCAATGACGGTTGGGGCTCGAGAT 931
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Db        788 GTATTTTCAATGGTTGTTCCAGCCAATGGGGTGCTCCCAATGACGGTTGGGGCTCAAGAT 847

Qy        932 ACGGTGGTATTTCTTCTGCATCTGACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTT 991
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Db        848 ACGGTGGTATTTCTTCTGCATCTGACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTT 907

Qy        992 GTAAATGGAGATTCAACTGGTTCAAGAACGCTGATAACCCAAGCATGACTTACAAGGAAG 1051
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Db        908 GTAAATGGAGATTCAACTGGTTCAAGAACGCTGATAACCCAAGCATGACTTACAAGGAAG 967

Qy       1052 TTACCTGTCCCAAGGAAATCACCGCCAAGACAGGTTGTTCAAGAAAATAA 1101
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Db        968 TTACCTGTCCTAAGGAAATCACCGCCAAGACAGGTTGTTCAAGAAAATAA 1017
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RESULT 3
US-10-380-420-1
; Sequence 1, Application US/10380420
; GENERAL INFORMATION:
; APPLICANT: Meiji Seika Kaisha, Ltd.
; TITLE OF INVENTION: METHOD OF DEINKING WASTE PAPER USING CELLULASE WITHOUT LOWERING P
; TITLE OF INVENTION: STRENGTH AND EVALUATION METHOD THEREOF
; FILE REFERENCE: VX032516 PCT
; CURRENT APPLICATION NUMBER: US/10/380,420
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: PCT/JP01/08017
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Rhizopus oryzae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1017)
; OTHER INFORMATION:
US-10-380-420-1

Query Match 69.3%; Score 763; DB 8; Length 1017;
Best Local Similarity 90.3%; Pred. No. 1.7e-219;
Matches 858; Conservative 0; Mismatches 35; Indels 57; Gaps 2;

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Qy        209 CTTCTGAATGTAGCAAGTTGTATGGTCAATGTGGTGGTAAGGACTGGAATGGCCCTACTT 268
              || |||||||||||| |||||||||||||||||||||||| ||||||||||||||||||
Db         68 CTGCTGAATGTAGCAAATTGTATGGTCAATGTGGTGGTAAGAACTGGAATGGCCCTACTT 127

Qy        269 GTTGCGAATCTGGATCCACCTGTAAAGTAAGCAACGATTACTACTCTCAATGTCTTGCCC 328
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        128 GTTGTGAATCTGGATCCACCTGTAAAGTAAGCAACGATTACTACTCTCAATGTCTTCCCT 187

Qy        329 CTGAAAGCAATGGCAATAAAACTTCTGAAAGCGCTCATAAAACGACT------------- 375
              ||| ||||| |||||||||| |||||||||| ||||| || | ||||
Db        188 CTGGAAGCAGTGGCAATAAATCTTCTGAAAGTGCTCACAAGAAGACTACCACTGCTGCTC 247

Qy        376 -------------------------------ACTACCACTGCTCCCGCTAAGGAAATTA 403
                                              |||||||||||||| |||||| | | ||
Db        248 ACAAGAAGACTACTACCGCTGCTCATAAAAAGACTACCACTGCTCCTGCTAAGAAGACTA 307

Qy        404 CAACTACTGCCAAAGCTTCAAACTCTTCTAACTCT------------AGCGGCAAATACT 451
              ||||| |||||||||||| | | |||||||||||             |||||||||| |
Db        308 CAACTGTTGCCAAAGCTTCCACCCCTTCTAACTCTAGCTCTAGCTCCAGCGGCAAATATT 367

Qy        452 CCATTGTCTCTGGTGGTGCCTCTGGTAACGGTGTCACTACTCGTTATTGGGATTGCTGTA 511
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CCGCTGTCTCTGGTGGTGCCTCTGGTAACGGTGTCACTACTCGTTATTGGGATTGCTGTA 427

Qy        512 AGGCCTCCTGTAGCTGGCCCGGTAAGGCCAATGTCAGTTCTCCTGTCAAGTCCTGTAACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 AGGCCTCCTGTAGCTGGCCCGGTAAGGCCAATGTCAGTTCTCCTGTCAAGTCCTGTAACA 487

Qy        572 AAGATGGTGTCACTGCCCTTAGTGACAGCAATGTCCAAAGTGGCTGTAACGGTGGTAACA 631
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        488 AAGATGGTGTCACTGCCCTTAGTGACAGCAATGCCCAAAGTGGCTGTAACGGTGGTAACA 547

Qy        632 GTTACATGTGTAACGACAACCAGCCTTGGGCTGTAAACGATAATCTTGCCTATGGTTTCG 691
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Db        548 GTTACATGTGTAACGACAACCAACCTTGGGCTGTAAACGACAACCTTGCCTATGGTTTCG 607

Qy        692 CTGCTGCTGCCATCAGTGGTGGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTA 751
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Db        608 CTGCTGCTGCCATCAGTGGTGGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTA 667

Qy        752 CTTTCACTTCTACCTCTGTTGCTGGTAAGAAGATGGTTATCCAAGTCACTAACACTGGTG 811
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Db        668 CTTTCACTTCTACCTCTGTTGCTGGTAAGAAGATGGTTGTCCAAGTCACTAACACTGGTG 727

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Db        728 GTGATCTTGGCTCCTCTACTGGTGCTCACTTTGACTTGCAAATGCCCGGTGGTGGTGTTG 787

Qy        872 GTATTTTCAATGGTTGCTCCAAGCAATGGGGTGCTCCCAATGACGGTTGGGGCTCGAGAT 931
              |||||||||||||||| ||||  ||||||||||||||||||||||||||||||| ||||
Db        788 GTATTTTCAATGGTTGTTCCAGCCAATGGGGTGCTCCCAATGACGGTTGGGGCTCAAGAT 847

Qy        932 ACGGTGGTATTTCTTCTGCATCTGACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTT 991
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 ACGGTGGTATTTCTTCTGCATCTGACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTT 907

Qy        992 GTAAATGGAGATTCAACTGGTTCAAGAACGCTGATAACCCAAGCATGACTTACAAGGAAG 1051
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GTAAATGGAGATTCAACTGGTTCAAGAACGCTGATAACCCAAGCATGACTTACAAGGAAG 967

Qy       1052 TTACCTGTCCCAAGGAAATCACCGCCAAGACAGGTTGTTCAAGAAAATAA 1101
              |||||||||| ||||||||||||||||||||||||||||||||||||||
Db        968 TTACCTGTCCTAAGGAAATCACCGCCAAGACAGGTTGTTCAAGAAAATAA 1017
```

RESULT 4
US-09-807-933B-6
; Sequence 6, Application US/09807933B
; GENERAL INFORMATION:
; APPLICANT: MEIJI SEIKA KAISHA, LTD.
; TITLE OF INVENTION: Endoglucanase and cellulase composition containing the
; TITLE OF INVENTION: same
; FILE REFERENCE: 121659PX
; CURRENT APPLICATION NUMBER: US/09/807,933B
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: JP302387/1998
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1083
; TYPE: DNA
; ORGANISM: Rhizopus oryzae CP96001
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(69)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (70)..(1083)
US-09-807-933B-6

Query Match 47.1%; Score 519; DB 6; Length 1083;
Best Local Similarity 69.7%; Pred. No. 8.9e-146;
Matches 772; Conservative 0; Mismatches 305; Indels 30; Gaps 4;

```
Qy          1 ATGAAGTTTATTACTATTACCTCTTCCGCTCTCTTGGCTCTCGCCCTTGGTACTGAAATG 60
              ||||||||  |||| ||| |||| |||||| ||||||| || ||| | ||||||||||||
Db          1 ATGAAGTTCCTTACCATTGCCTCCTCCGCTATCTTGGCACTTGCCGTCGGTACTGAAATG 60

Qy         61 GCCTCTGCTGCTAAATGTAGCAAGCTGTATGGTCAATGTGGTGGTAAGGACTGGAATGGC 120
              |||  ||||||| ||||||||||||    ||     ||||||||||||||| ||||| ||||
Db         61 GCCCATGCTGCTGAATGTAGCAAGGCTTACTACCAATGTGGTGGTAAGAACTGGGATGGA 120

Qy        121 CCTACTTGTTGCGAATCTGGATCCACCTG------TAAAGTAAGCAACGATTACTACTCT 174
              ||||| || || |||||||| || || ||       | |       |||   || ||||||
Db        121 CCTACCTGCTGTGAATCTGGCTCTACTTGCGTTGATTATCCTGACAATCCTTTCTACTCC 180
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Qy        175 CAATGTCTTGCCCCTGAAAGCAACGGCAATAAGTCTTCTGAATGTAGCAAGTTGTATGGT 234
              |||||| || ||  ||||| |  |  |  |           | |  |||          |
Db        181 CAATGTGTTCCCAATGAAAACCTCACCTCCACTAACAAATCTTCTCACAAAACCACCACT 240

Qy        235 CAATGTGGTGGTAAGGACTGGAATGGCCCTACTTGTTGCGAATCTGGATCCACCTGTAAA 294
                 |||  ||| |     |       |||   ||| | |         ||||   | ||
Db        241 ACTGAGAGTGCCAAGAAGACTACCACTACTAAAGGTTCCAAGAAGACCACCACTACTGAA 300

Qy        295 GTAAGCAACGATTACTACTCTCAATGTCTTGCCCCTGAAAGCAATGGCAATAAAACTTCT 354
              |     ||  |   |  | ||     | ||    | | |         | ||| ||
Db        301 GCCTCTAAGAAGACCACCACTACTGAAGCTTCCAAGAAGACC---------ACCACTACT 351

Qy        355 GAAAGCGCTCATAAAACGACTACTACCACTGCTCCCGCTAAGGAAATTACAACTACTGCC 414
              |||  | || | || || || ||||| |||      |||          ||||  ||
Db        352 GAAGCCTCTAAGAAGACCACCACTACTACTAAGAAGGCT----------TCTACCTCC 399

Qy        415 AAAGCTTCAAACTCTTCTAACTCTAGCGGCAAATACTCCATTGTCTCTGGTGGTGCCTCT 474
              |  | ||    |||||||    ||      || ||||||  ||||||||||||||||||
Db        400 ACTTCCTCTTCCTCTTCTTCTGCTTCTACAAACTACTCCGCTGTCTCTGGTGGTGCCTCC 459

Qy        475 GGTAACGGTGTCACTACTCGTTATTGGGATTGCTGTAAGGCCTCCTGTAGCTGGCCCGGT 534
              ||||| ||||  || ||||| || |||||||| |||||| | || || || ||||||||||
Db        460 GGTAATGGTGAAACCACTCGCTACTGGGATTGTTGTAAGCCTTCTTGCAGTTGGCCCGGT 519

Qy        535 AAGGCCAATGTCAGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCACTGCCCTTAGT 594
              |||||  ||||||  || |||||     |||||||||| ||||||   |||  |||  |
Db        520 AAGGCTGATGTCACCTCCCCTGTTGGCTCCTGTAACAAGGATGGTAAGACT---CTTGCT 576

Qy        595 GACAGCAATGTCCAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTAACGACAACCAG 654
              || | |||    ||||  ||||||  ||||||| ||| |||  |||||  |||| || ||
Db        577 GATAACAACACTCAAAACGGCTGTGTTGGTGGTAGCAGCTACACCTGTAATGACAATCAA 636

Qy        655 CCTTGGGCTGTAAACGATAATCTTGCCTATGGTTTCGCTGCTGCTGCCATCAGTGGTGGT 714
              ||||||| ||| | |||  | |||||||| |||||||| |||||| ||||   |||||||
Db        637 CCTTGGGTTGTTAGCGACGACCTTGCCTACGGTTTCGCCGCTGCTTCCATTTCTGGTGGT 696

Qy        715 GGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTACCTCTGTTGCT 774
              | ||| ||   ||||| ||| | |||||||||||  || |||||  |||||  | ||
Db        697 AGCGAAGCTACTTGGTGTTGTGCCTGTTTCGAACTCACATTCACCTCTACTGCCGTCAAG 756

Qy        775 GGTAAGAAGATGGTTATCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCTACTGGT 834
              |||||||||||||| | |||||  || |||||||||  ||| ||||||||   ||||||
Db        757 GGTAAGAAGATGGTTGTTCAAGTAACCAACACTGGTTCTGACCTTGGCTCTAACACTGGT 816

Qy        835 GCTCACTTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATGGTTGCTCCAAG 894
              |||||||||||||||||||||||||||||||||||||||||| | |||||||||  |||
Db        817 GCTCACTTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATCTACAATGGTTGTGCCACT 876

Qy        895 CAATGGGGTGCTCCCAATGACGGTTGGGGCTCGAGATACGGTGGTATTTCTTCTGCATCT 954
              ||||||||||||||||  || |||||||  | |||||||| ||| ||||||||| |||
Db        877 CAATGGGGTGCTCCCACCGATGGTTGGGGTGCAAGATACGGCGGTGTTTCTTCTGCCTCT 936

Qy        955 GACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAACTGGTTC 1014
              ||||| ||||  |||||||| || || |||||||||||||| |||||||||  |||||||
Db        937 GACTGTTCTAACCTTCCTTCTGCCCTTCAAGCTGGTTGTAAGTGGAGATTCGGCTGGTTC 996

Qy        1015 AAGAACGCTGATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCCAAGGAAATCACC 1074
               || |||||||||||||| |||||| |||||  |||||||||||||||||||  |||||
Db         997 AAAAACGCTGATAACCCAACCATGACCTACAAACAAGTTACCTGTCCCAAGGCTATCACT 1056

Qy        1075 GCCAAGACAGGTTGTTCAAGAAAATAA 1101
               |||||| | || ||||||||||||||||
Db        1057 GCCAAGTCTGGCTGTTCAAGAAAATAA 1083
```

RESULT 5
US-09-807-933B-13
; Sequence 13, Application US/09807933B
; GENERAL INFORMATION:
; APPLICANT: MEIJI SEIKA KAISHA, LTD.
; TITLE OF INVENTION; Endoglucanase and cellulase composition containing the
; TITLE OF INVENTION: same
; FILE REFERENCE: 121659PX
; CURRENT APPLICATION NUMBER: US/09/807,933B
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: JP302387/1998
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 1043
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (16)..(84)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (84)..(1043)
; OTHER INFORMATION: Codon-optimized sequence corresponding to RCE I protein
; OTHER INFORMATION: (SEQ. ID NO:2)
US-09-807-933B-13

Query Match 38.3%; Score 421.2; DB 6; Length 1043;
Best Local Similarity 72.4%; Pred. No. 3e-116;
Matches 565; Conservative 0; Mismatches 203; Indels 12; Gaps 1;

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Qy        334 AGCAATGGCAATAAAACTTCTGAAAGCGCTCATAAAACGACTACTACCACTGCTCCCGCT 393
              | |  || | | || |  |     | |||   | | | ||  ||||| || ||||||||
Db        253 ACCGCTGCCCACAAGAAGACCACGACCGCCGCTCACAAGAAGACTACGACCGCTCCCGCC 312

Qy        394 AAGGAAATTACAACTACTGCCAAAGCTTCAAACTCTTCTAACTCTAGCGGC--------- 444
              ||| | |  || ||    |||||  |||| |  | || |||| ||| ||
Db        313 AAGAAGACCACGACCGTCGCCAAGGCTTCGACTCCGTCCAACTCGAGCAGCTCGTCTTCG 372

Qy        445 ---AAATACTCCATTGTCTCTGGTGGTGCCTCTGGTAACGGTGTCACTACTCGTTATTGG 501
                  || |||  | ||||  ||||| ||    || |||||| |||||||| || || |||
Db        373 GGAAAGTACAGCGCTGTCAGCGGTGGCGCTAGCGGCAACGGCGTCACTACCCGCTACTGG 432

Qy        502 GATTGCTGTAAGGCCTCCTGTAGCTGGCCCGGTAAGGCCAATGTCAGTTCTCCTGTCAAG 561
              || ||||| ||||| || ||    |||||||| |||| || ||||| || ||||||||||
Db        433 GACTGCTGCAAGGCTTCGTGCTCGTGGCCCGGCAAGGCTAACGTCAGCTCGCCTGTCAAG 492

Qy        562 TCCTGTAACAAAGATGGTGTCACTGCCCTTAGTGACAGCAATGTCCAAAGTGGCTGTAAC 621
              ||||| ||||| || || ||||| || ||||| |||  ||| | |||     ||||| |||
Db        493 TCCTGCAACAAGGACGGCGTCACCGCTCTTAGCGACTCCAACGCCCAGTCCGGCTGCAAC 552

Qy        622 GGTGGTAACAGTTACATGTGTAACGACAACCAGCCTTGGGCTGTAAACGATAATCTTGCC 681
              || || |||   |||||||| |||||||||||||| |||||||| ||||| || |||||
Db        553 GGCGGCAACTCCTACATGTGCAACGACAACCAGCCATGGGCTGTCAACGACAACCTTGCT 612

Qy        682 TATGGTTTCGCTGCTGCTGCCATCAGTGGTGGTGGTGAATCTCGCTGGTGCTGTTCTTGT 741
              || |||||||||| |||||||| || || ||||| ||     |||||||||| || ||
Db        613 TACGGTTTCGCTGCCGCTGCCATTAGCGGCGGTGGCGAGAGCCGCTGGTGCTGCTCCTGC 672

Qy        742 TTCGAACTTACTTTCACTTCTACCTCTGTTGCTGGTAAGAAGATGGTTATCCAAGTCACT 801
              ||||| || || ||||| || |||   |||||||| |||||||||| |||| ||||||
Db        673 TTCGAGCTCACCTTCACCTCCACCAGCGTTGCTGGCAAGAAGATGGTCGTCCAGGTCACC 732

Qy        802 AACACTGGTGGTGATCTTGGCTCCTCTACTGGTGCTCACTTTGACTTGCAAATGCCCGGT 861
              |||||||| ||||| ||||||  ||| || ||||| ||||  | || ||||||||
Db        733 AACACTGGCGGTGACCTTGGCAGCTCGACCGGTGCCCACTTCGATCTCCAGATGCCCGGC 792

Qy        862 GGTGGTGTTGGTATTTTCAATGGTTGCTCCAAGCAATGGGGTGCTCCCAATGACGGTTGG 921
              || || || || || ||||| || |||||    || ||||| |||||||| ||||| |||
Db        793 GGCGGCGTCGGCATCTTCAACGGATGCTCGTCCCAGTGGGGCGCTCCCAACGACGGCTGG 852

Qy        922 GGCTCGAGATACGGTGGTATTTCTTCTGCATCTGACTGCTCTAGTCTTCCTTCCGCACTC 981
              |||||| | ||||| || ||    || ||    |||||||     || ||  ||| |||
Db        853 GGCTCGCGCTACGGCGGCATCAGCTCCGCCAGCGACTGCTCGTCCCTCCCCAGCGCCCTC 912

Qy        982 CAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAACGCTGATAACCCAAGCATGACT 1041
              || || || || || ||| | |||||||||||||||||||| || |||||   ||||||
Db        913 CAGGCCGGCTGCAAGTGGCGCTTCAACTGGTTCAAGAACGCCGACAACCCGTCCATGACC 972

Qy        1042 TACAAGGAAGTTACCTGTCCCAAGGAAATCACCGCCAAGACAGGTTGTTCAAGAAAATAA 1101
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                ||||||||  ||  |||||  ||||||||  ||||||||  |||||  ||  ||  ||   |  ||  |||
Db        973 TACAAGGAGGTCACCTGCCCCAAGGAGATCACCGCTAAGACCGGATGCTCGCGCAAGTAA 1032


RESULT 6
US-09-807-933B-10
; Sequence 10, Application US/09807933B
; GENERAL INFORMATION:
;  APPLICANT: MEIJI SEIKA KAISHA, LTD.
;  TITLE OF INVENTION: Endoglucanase and cellulase composition containing the
;  TITLE OF INVENTION:  same
;  FILE REFERENCE: 121659PX
;  CURRENT APPLICATION NUMBER: US/09/807,933B
;  CURRENT FILING DATE:  2002-04-18
;  PRIOR APPLICATION NUMBER: JP302387/1998
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 113
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 1164
;   TYPE: DNA
;   ORGANISM: Mucor circinelloides CP99001
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: (1)..(66)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (67)..(1164)
US-09-807-933B-10

  Query Match             35.4%;  Score 390.2;  DB 6;  Length 1164;
  Best Local Similarity   64.2%;  Pred. No. 7.3e-107;
  Matches  715;  Conservative    0;  Mismatches  308;  Indels   90;  Gaps    5;

Qy          67 GCTGCTAAATGTAGCAAGCTGTATGGTCAATGTGGTGGTAAGGACTGGAATGGCCCTACT 126
               ||||||   ||  |||    | ||||||||||||||||||  |  | |||||  ||| |||||
Db          64 GCTGCTTCTTGCAGCTCTGTCTATGGTCAATGTGGTGGCATTGGCTGGACTGGTCCTACA 123

Qy         127 TGTTGCGAATCTGGATCCACCTGTAAAGTAAGCAACGAT------TACTACTCTCAATGT 180
               |||||  ||  |||||||  ||||||||||     ||  |||      ||  ||  |||||||||
Db         124 TGTTGTGATGCTGGATCGACCTGTAAAGCTCAAAAGGATAACAAATATTATTCTCAATGT 183

Qy         181 CTTGCCCCTGAAAGCAACGGCAATAAGTCTTCTGAATGTAGCAAGTTGTATGGTCAATGT 240
                || ||       |          |       ||  ||   ||||||      | |||  |||||||
Db         184 ATTCCCAAACCCAAGGGTTCCTCCTCATCATCATCATGTAGTTCCGTCTATAGTCAATGC 243

Qy         241 GGTGGTAAGGACTGGAATGGCCCTACTTGTTGCGAATCTGGATCCACCTG------TAAA 294
               |||||  |   |  ||||  |||  |||||  |||||  |||   |||  ||  ||  ||       | ||
Db         244 GGTGGCATTGGATGGAGTGGACCTACCTGTTGTGAAAGTGGCTCTACTTGCGTTGCTCAA 303

Qy         295 GTAAGCAACGATTACTACTCTCAATGTCTTGCCCCTGAAAGCAATGGCAATAAAACTTCT 354
               | | |||||  | |||||||||||||||||||  ||         ||  |   ||||      |
Db         304 GAAGGCAACAAATACTACTCTCAATGTCTTCCCGGATCCCACAGTAACAATGCTGGTAAC 363

Qy         355 GAAAGCGCTCATAAAACGACTACTACC----------------------------------- 381
               |  |||       ||  |  |||   |||||
Db         364 GCTAGCAGCACCAAGAAGACATCTACCAAGACATCTACTACCACCGCCAAGGCTACTGCT 423

Qy         382 ---------------------------------ACTGCTCCCGCTAAGGAAATTACAACT 408
                                                ||     |  |||   | |  ||  |||
Db         424 ACTGTCACCACCAAGACAGTAACCAAGACAACTACCAAGACAACTACCAAGACTAGCACT 483

Qy         409 ACTGCCAAAGCTTCAAACTCTTCTAACTCTAGCGGCAAATACTCCATTGTCTCTGGTGGT 468
               ||||||   |||||  |  ||  |   |||   |     |||     |  ||||||| |||
Db         484 ACTGCCGCTGCTTCTACTTCCACCTCTTCTTCTGCTGGTTACAAGGTCATCTCTGGCGGT 543

Qy         469 GCCTCTGGTAACGGTGTCACTACTCGTTATTGGGATTGCTGTAAGGCCTCCTGTAGCTGG 528
               |||||  |  |||  |||  ||||||||||||||||||  |||||  ||  ||  ||  ||||||
Db         544 AAATCTGGCAGTGGTTCCACAACTCGTTATTGGGATTGTTGTAAAGCTTCTTGCAGCTGG 603

Qy         529 CCCGGTAAGGCCAATGTCAGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCACTGCC 588
               ||  ||  ||  ||   |||||  |  ||||||  |  |||||  |     |||||  ||  ||
Db         604 CCTGGAAAAGCTTCTGTCACTGGTCCTGTTGACACCTGTGCCTCCAATGGTATCTCT--- 660

Qy         589 CTTAGTGACAGCAATGTCCAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTAACGAC 648
                  |    ||    |||||  ||||||||  ||||||||||||||   |||  ||||||||||  ||
Db         661 TTATTAGATGCCAATGCTCAAAGTGGTTGTAACGGTGGTAATGGTTTCATGTGTAACAAC 720

Qy         649 AACCAGCCTTGGGCTGTAAACGATAATCTTGCCTATGGTTTCGCTGCTGCTGCCATCAGT 708
               |||||  ||||||||||  ||  |||  |  ||  ||  ||  ||||||||||||||   |  ||    |
Db         721 AACCAACCTTGGGCTGTCAATGATGAGCTCGCTTACGGTTTCGCTGCTGCCTCTATTGCT 780

Qy         709 GGTGGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTACCTCT 768
               ||        |||  ||  |  ||||||  |||    ||||   |||  |  ||  ||||||||||   |  ||
Db         781 GGCTCCAACGAAGCTGGATGGTGTTGTGGCTGTTATGAATTGACCTTCACTTCTGGCGCT 840

Qy         769 GTTGCTGGTAAGAAGATGGTTATCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCT 828
               |  |  ||||  ||||||||||||  |  |||||  ||  |||||  |||||  |||  |  |||||
Db         841 GCTTCTGGAAAGAAGATGGTTGTTCAAGTTACCAACACCGGTGGCGATTTAGGCTC---- 896

Qy         829 ACTGGTGCTCACTTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATGGTTGC 888
                     |   ||||||||  ||||||||||||||||||||  ||||||||  ||||||||  ||
Db         897 -----TAACCACTTTGATTTGCAAATGCCCGGTGGTGGCGTTGGTATCTTCAATGGCTGT 951

Qy         889 TCCAAGCAATGGGGTGCTCCCAATGACGGTTGGGGCTCGAGATACGGTGGTATTTCTTCT 948
                  |     ||||||||  ||||||||||  ||  |||||   |  |||||  ||||||  |     |||
Db         952 GCTGCTCAATGGGGCGCTCCCAATGATGGCTGGGGAGCTAGATATGGTGGTGTCAGCTCT 1011

Qy         949 GCATCTGACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAAC 1008
               |  ||||||||   |   ||||||  ||  ||  ||  ||||||||||||||||||||||||||||
Db        1012 GTCTCTGACTGTGCCTCTCTTCCCTCTGCTCTTCAAGCTGGTTGTAAATGGAGATTCAAC 1071

Qy        1009 TGGTTCAAGAACGCTGATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCCAAGGAA 1068
               ||||||||||||  ||||||||||  |  ||||||  |  ||||||||||||||||||     |||
Db        1072 TGGTTCAAGAACTCTGATAACCCTACCATGACCTTCAAGGAAGTTACCTGTCCTGCTGAA 1131

Qy        1069 ATCACCGCCAAGACAGGTTGTTCAAGAAAATAA 1101
                 |  ||  |      |||||||   ||||||  |||
Db        1132 TTAACTACTCGCTCAGGTTGCGAAAGAAAGTAA 1164


RESULT 7
US-09-807-933B-8
; Sequence 8, Application US/09807933B
; GENERAL INFORMATION:
;  APPLICANT: MEIJI SEIKA KAISHA, LTD.
;  TITLE OF INVENTION: Endoglucanase and cellulase composition containing the
;  TITLE OF INVENTION:  same
;  FILE REFERENCE: 121659PX
;  CURRENT APPLICATION NUMBER: US/09/807,933B
;  CURRENT FILING DATE:  2002-04-18
;  PRIOR APPLICATION NUMBER: JP302387/1998
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 113
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 1017
;   TYPE: DNA
;   ORGANISM: Mucor circinelloides CP99001
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: (1)..(66)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (67)..(1017)
US-09-807-933B-8

  Query Match             33.4%;  Score 367.4;  DB 6;  Length 1017;
  Best Local Similarity   70.9%;  Pred. No. 5.3e-100;
  Matches  520;  Conservative    0;  Mismatches  201;  Indels   12;  Gaps    2;

Qy         369 AACGACTACTACCACTGCTCCCGCTAAGGAAATTACAACTACTGCCAAAGCTTCAAACTC 428
               |||  |  ||  ||  ||     |  |||   |  |  ||  |||||||||   |||||  |  ||
Db         297 AACCAAGACAACTACCAAGACAACTACCAAGACTAGCACTACTGCCGCTGCTTCTACTTC 356

Qy         429 TTCTAACTCTAGCGGCAAATACTCCATTGTCTCTGGTGGTGCCTCTGGTAACGGTGTCAC 488
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Db        357 CACCTCTTCTTCTGCTGGTTACAAGGTCATCTCTGGCGGTAAATCTGGCAGTGGTTCCAC 416
Qy        489 TACTCGTTATTGGGATTGCTGTAAGGCCTCCTGTAGCTGGCCCGGTAAGGCCAATGTCAG 548
Db        417 AACTCGTTATTGGGATTGTTGTAAAGCTTCTTGCAGCTGGCCTGGAAAAGCTTCTGTCAC 476
Qy        549 TTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCACTGCCCTTAGTGACAGCAATGTCCA 608
Db        477 TGGTCCTGTTGACACCTGTGCCTCCAATGGTATCTCT---TTATTAGATGCCAATGCTCA 533
Qy        609 AAGTGGCTGTAACGGTGGTAACAGTTACATGTGTAACGACAACCAGCCTTGGGCTGTAAA 668
Db        534 AAGTGGTTGTAACGGTGGTAATGGTTTCATGTGTAACAACAACCAACCTTGGGCTGTCAA 593
Qy        669 CGATAATCTTGCCTATGGTTTCGCTGCTGCTGCCATCAGTGGTGGTGGTGAATCTCGCTG 728
Db        594 TGATGAGCTCGCTTACGGTTTCGCTGCTGCCTCTATTGCTGGCTCCAACGAAGCTGGATG 653
Qy        729 GTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTACCTCTGTTGCTGGTAAGAAGATGGT 788
Db        654 GTGTTGTGGCTGTTATGAATTGACCTTCACTTCTGGCGCTGCTTCTGGAAAGAAGATGGT 713
Qy        789 TATCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCTACTGGTGCTCACTTTGACTT 848
Db        714 TGTTCAAGTTACCAACACCGGTGGCGATTTAGGCTC---------TAACCACTTTGATTT 764
Qy        849 GCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATGGTTGCTCCAAGCAATGGGGTGCTCC 908
Db        765 GCAAATGCCCGGTGGTGGCGTTGGTATCTTCAATGGCTGTGCTGCTCAATGGGGCGCTCC 824
Qy        909 CAATGACGGTTGGGGCTCGAGATACGGTGGTATTTCTTCTGCATCTGACTGCTCTAGTCT 968
Db        825 CAATGATGGCTGGGGAGCTAGATATGGTGGTGTCAGCTCTGTCTCTGACTGTGCCTCTCT 884
Qy        969 TCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAACGCTGATAA 1028
Db        885 TCCCTCTGCTCTTCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAACTCTGATAA 944
Qy       1029 CCCAAGCATGACTTACAAGGAAGTTACCTGTCCCAAGGAAATCACCGCCAAGACAGGTTG 1088
Db        945 CCCTACCATGACCTTCAAGGAAGTTACCTGTCCTGCTGAATTAACTACTCGCTCAGGTTG 1004
Qy       1089 TTCAAGAAAATAA 1101
Db       1005 CGAAAGAAAGTAA 1017
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RESULT 8
US-09-807-933B-12
; Sequence 12, Application US/09807933B
; GENERAL INFORMATION:
; APPLICANT: MEIJI SEIKA KAISHA, LTD.
; TITLE OF INVENTION: Endoglucanase and cellulase composition containing the
; TITLE OF INVENTION: same
; FILE REFERENCE: 121659PX
; CURRENT APPLICATION NUMBER: US/09/807,933B
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: JP302387/1998
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Phycomyces nitens CP99002
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(57)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (58)..(1041)
US-09-807-933B-12

Query Match 26.3%; Score 289.6; DB 6; Length 1041;
Best Local Similarity 64.3%; Pred. No. 1.7e-76;
Matches 471; Conservative 0; Mismatches 249; Indels 12; Gaps 2;

```
Qy        370 ACGACTACTACCACTGCTCCCGCTAAGGAAATTACAACTACTGCCAAAGCTTCAAACTCT 429
Db        322 ACTACTACCACCACCAAGACCACCACCAAGACCACCACCACCAAGGCTGCCACCACCACC 381
Qy        430 TCTAACTCTAGCGGCAAATACTCCATTGTCTCTGGTGGTGCCTCTGGTAACGGTGTCACT 489
Db        382 TCCTCTTCCAACACTGGCTACAGCCCCATTTCTGGTGGCTTCTCTGGAAACGGTCGCACT 441
Qy        490 ACTCGTTATTGGGATTGCTGTAAGGCCTCCTGTAGCTGGCCCGGTAAGGCCAATGTCAGT 549
Db        442 ACCCGCTACTGGGATTGCTGCAAGCCCTCTTGCGCCTGGGACGGAAAGGCTTCTGTAACT 501
Qy        550 TCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCACTGCCCTTAGTGACAGCAATGTCCAA 609
Db        502 AAGCCTGTACTCACCTGTGCCAAGGATGGTGTCA---GCCGTCTCGGTTCCGATGTCCAG 558
Qy        610 AGTGGCTGTAACGGTGGTAACAGTTACATGTGTAACGACAACCAGCCTTGGGCTGTAAAC 669
Db        559 AGCGGTTGCGTCGGCGGCCAGGCCTACATGTGCAATGACAACCAGCCCTGGGTTGTCAAT 618
Qy        670 GATAATCTTGCCTATGGTTTCGCTGCTGCTGCCATCAGTGGTGGTGGTGAATCTCGCTGG 729
Db        619 GACGACCTTGCCTACGGTTTCGCTGCTGCCAGTCTCGGTAGCGCCGGTGCCTCTGCATTC 678
Qy        730 TGCTGTTCTTGTTTCGAACTTACTTTCACTTCTACCTCTGTTGCTGGTAAGAAGATGGTT 789
Db        679 TGCTGCGGCTGTTACGAGCTTACCTTCACCAACACTGCTGTCGCTGGCAAGAAGTTTGTC 738
Qy        790 ATCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCTACTGGTGCTCACTTTGACTTG 849
Db        739 GTCCAGGTCACCAACACCGGTGATGATCTCAGCACCAAC---------CACTTTGATTTG 789
Qy        850 CAAATGCCCGGTGGTGGTGTTGGTATTTTCAATGGTTGCTCCAAGCAATGGGGTGCTCCC 909
Db        790 CAGATGCCCGGCGGTGGTGTCGGCTACTTCAACGGCTGCCAGTCCCAGTGGAACACCAAC 849
Qy        910 AATGACGGTTGGGGCTCGAGATACGGTGGTATTTCTTCTGCATCTGACTGCTCTAGTCTT 969
Db        850 ACCGATGGCTGGGGTGCTCGCTATGGCGGTATTAGCTCTATTTCAGAGTGCGACAAGCTT 909
Qy        970 CCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAACGCTGATAAC 1029
Db        910 CCTACCCAGTTGCAGGCTGGTTGCAAGTGGAGATTCGGATGGTTCAAGAACGCTGACAAC 969
Qy       1030 CCAAGCATGACTTACAAGGAAGTTACCTGTCCCAAGGAAATCACCGCCAAGACAGGTTGT 1089
Db        970 CCAGAGGTCACCTTCAAGGCTGTTACTTGCCCTGCCGAGATCATTGCCAAGACTGGTTGC 1029
Qy       1090 TCAAGAAAATAA 1101
Db       1030 GAGCGCAAGTAA 1041
```

RESULT 9
US-10-369-493-27891
; Sequence 27891, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039

```
;  PRIOR FILING DATE: 2002-02-21
;  NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 27891
;   LENGTH: 890
;   TYPE: DNA
;   ORGANISM: Neurospora crassa
US-10-369-493-27891

  Query Match             10.0%;  Score 109.8;  DB 8;  Length 890;
  Best Local Similarity   53.9%;  Pred. No. 3.2e-22;
  Matches  369;  Conservative    0;  Mismatches  242;  Indels   74;  Gaps    4;

Qy        466 GGTGCCTCTGGTAACGGTGTCACTACTCGTTATTGGGATTGCTGTAAGGCCTCCTGTAGC 525
              | ||| || ||   |||     | ||  | |||||||| ||||| ||  | || ||   |
Db         19 GCTGCTTCCGGATCCGGCCAGTCCACCAGATATTGGGACTGCTGCAAACCATCTTGCTCC 78

Qy        526 TGGCCCGGTAAGGCCAATGTCAGTTCTCCTGTCAAGTCCTGTAACAAAGATGGTGTCACT 585
              ||| |||| |||||   |||||     || |||    | ||  ||  | |      ||
Db         79 TGGTCCGGCAAGGCTCCTGTCAACCGACCCGTCCTCGCTTGCGACGCAAACAA---CAAC 135

Qy        586 GCCCTTAGTGACAGCAATGTCCAAAGTGGCTGTAACGGTGGTAACAGTTACATGTGTAAC 645
              |||| || |||  || |||| |   ||| ||| | || |||      ||||  |||  |
Db        136 CCCCTGAGCGACGCCAGTGTCAAGTCTGGATGTGATGGCGGTTCTGCATACACCTGTGCC 195

Qy        646 GACAACCAGCCTTGGGCTGTAAACGATAATCTTGCCTATGGTTTCGCTGCTGCTGCCATC 705
              |||||   || ||||| || |||||  | ||  |||| || || || ||  |      ||
Db        196 AACAACTCACCATGGGCGGTGAACGACCAGCTCTCCTACGGCTTTGCCGCCACGAAACTC 255

Qy        706 AGTGGTGGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAA----------------- 747
              ||||||||    || ||    |||||||| | ||||  |
Db        256 AGTGGTGGAACCGAGTCATCTTGGTGCTGTGCCTGTTATGCGTGAGTTTCTCTTCAACTC 315

Qy        748 ----------------------------------CTTACTTTCACTTCTACCTCTGTTG 772
                                               ||||| ||||||||   | ||||||
Db        316 TTGGGTATCACTCGATGGCTAACTTTTACTGCAGCCTTACCTTCACTTCGGGCCCTGTTG 375

Qy        773 CTGGTAAGAAGATGGTTATCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCTACTG 832
              |||| ||||   |||| | ||    || |  || || |||||||| ||||||
Db        376 CTGGCAAGACCTTGGTCGTTCAGTCTACCAGTACCGGCGGTGATCTCGGCTCCAAC---- 431

Qy        833 GTGCTCACTTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAATGGTTGCTCCA 892
                  ||||| ||  |  | |||||||| || || || ||  | ||  |||| ||
Db        432 -----CACTTCGATATCAACATGCCCGGCGGCGGCGTCGGCCTGTTTGATGGATGTAAAC 486

Qy        893 AGCAATGGGGTGCTCCCAATGACGGTTGGGGCTCGAGATACGGTGGTATTTCTTCTGCAT 952
              || |  || | || |   | || |           ||| || || ||    ||
Db        487 GACAGTTCGGCGGTCTCCCCGGCGCTCA---------ATATGGCGGCATCAGCTCCCGCA 537

Qy        953 CTGACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAACTGGT 1012
              | |||        | ||| |||| ||| |  | |||||  | ||| | ||| ||||||
Db        538 GCCAGTGCGACTCGTTCCCTGCCGCTCTCAAGCCCGGTTGCCAGTGGCGCTTCGACTGGT 597

Qy       1013 TCAAGAACGCTGATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCCAAGGAAATCA 1072
              || ||||||| |||||||| | | | || | |||| | ||    || ||    ||  |||
Db        598 TCCAGAACGCCGATAACCCGAACTTCACCTTCAAGCAGGTCCAATGCCCATCCGAGCTCA 657

Qy       1073 CCGCCAAGACAGGTTGTTCAAGAAA 1097
              |  ||   || || ||     ||||
Db        658 CATCCCGCACCGGCTGCAAGCGAAA 682


RESULT 10
US-10-205-189A-241
; Sequence 241, Application US/10205189A
; GENERAL INFORMATION:
;  APPLICANT: Andersen, Scott E.
;  APPLICANT:  Huesing, Joseph E.
;  APPLICANT:  Romano, Charles P.
;  APPLICANT:  Vetsch, Clayton S.
;  APPLICANT:  Hicks, Glenn R.
;  TITLE OF INVENTION: Nucleic Acid Sequences from Diabrotica virgifera virgifera
;  TITLE OF INVENTION:  LeConte and Uses thereof
;  FILE REFERENCE: 38-21(51497)C
;  CURRENT APPLICATION NUMBER: US/10/205,189A
;  CURRENT FILING DATE:  2002-07-24
;  PRIOR APPLICATION NUMBER: US 60/307,512
;  PRIOR FILING DATE: 2001-07-24
;  NUMBER OF SEQ ID NOS: 9112
; SEQ ID NO 241
;   LENGTH: 423
;   TYPE: DNA
;   ORGANISM: Diabrotica virgifera
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB3026-024-Q1-E1-B9
US-10-205-189A-241

  Query Match             8.8%;  Score 96.8;  DB 8;  Length 423;
  Best Local Similarity   58.2%;  Pred. No. 2e-18;
  Matches  233;  Conservative    0;  Mismatches  152;  Indels   15;  Gaps    3;

Qy        685 GGTTTCGCTGCTGCTGCCATCAGTGGTGGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTC 744
              |||||  | ||||||  |  |||||   ||   |||       ||  || ||  ||||||||
Db         32 GGTTTTGGTGCTGCATCTTTCAGTAACGGAATTGATGTATCCTTATGTTGCGCTTGTTTC 91

Qy        745 GAACTTACTTTCACTTCTACCTCTGTTGCTGGTAAGAAGATGGTTATCCAAGTCACTAAC 804
              |||||  ||||    |       || |    |||||||||  |  | |||||  || ||
Db         92 TTACTTAGCTTCAAAGAT---CAAATTTCAAACAAGAAGATGATCGTACAAGTTACAAAT 148

Qy        805 ACTGGTGGTGATCTTGGCTCCTCTACTGGTGCTCACTTTGACTTGCAAATGCCCGGTGGT 864
              ||||||  ||||  |  |           |  |  |||  || ||| |      | |||||  |||
Db        149 ACTGGTTCTGATTTAAG---------TCATAATCATTTCGACATCGCTCTTCCCGGAGGT 199

Qy        865 GGTGTTGGTATTTTCA---ATGGTTGCTCCAAGCAATGGGGTGCTCCCAATGACGGTTGG 921
              |||||||| |||||||   | |||||      | ||||||  |||  ||      ||||||||
Db        200 GGTGTTGGAATTTTCACACAAGGTTGTCATGACCAATGGAATGCCCCATGGAACGGTTGG 259

Qy        922 GGCTCGAGATACGGTGGTATTTCTTCTGCATCTGACTGCTCTAGTCTTCCTTCCGCACTC 981
              ||       ||| |||||  ||  |       |  || ||  ||| |||||||    ||  |
Db        260 GGTGACCAATATGGTGGAGTTCATAACAGAGGGGAATGTGCTACTCTTCCTCAAGCCTTA 319

Qy        982 CAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAACGCTGATAACCCAAGCATGACT 1041
              ||  |||| ||  | |  |||||  | | | | |||| |||    || ||| | |||  |
Db        320 CAGTCTGGATGCTACTTCAGATTTGATTTCTACCAGAATGCTACCAATCCACGAATGCAT 379

Qy       1042 TACAAGGAAGTTACCTGTCCCAAGGAAATCACCGCCAAGA 1081
              | | | |||||      | ||    ||||||   |||| ||
Db        380 TTCGACGAAGTCTAAGGCCCTGCTGAAATCGTTGCCAGGA 419


RESULT 11
US-10-205-189A-233
; Sequence 233, Application US/10205189A
; GENERAL INFORMATION:
;  APPLICANT: Andersen, Scott E.
;  APPLICANT:  Huesing, Joseph E.
;  APPLICANT:  Romano, Charles P.
;  APPLICANT:  Vetsch, Clayton S.
;  APPLICANT:  Hicks, Glenn R.
;  TITLE OF INVENTION: Nucleic Acid Sequences from Diabrotica virgifera virgifera
;  TITLE OF INVENTION:  LeConte and Uses thereof
;  FILE REFERENCE: 38-21(51497)C
;  CURRENT APPLICATION NUMBER: US/10/205,189A
;  CURRENT FILING DATE:  2002-07-24
;  PRIOR APPLICATION NUMBER: US 60/307,512
;  PRIOR FILING DATE: 2001-07-24
;  NUMBER OF SEQ ID NOS: 9112
; SEQ ID NO 233
;   LENGTH: 627
;   TYPE: DNA
;   ORGANISM: Diabrotica virgifera
;   FEATURE:
;   OTHER INFORMATION: Clone ID: pGUT3409
US-10-205-189A-233

  Query Match             8.6%;  Score 94.6;  DB 8;  Length 627;
  Best Local Similarity   53.7%;  Pred. No. 1.1e-17;
```

```
  Matches  296;  Conservative    0;  Mismatches  234;  Indels   21;  Gaps    4;

Qy        465 TGGTGCCTCTGGTAACGGTGTCACTACTCGTTATTGGGATTGCTGTAAGGCCTCCTGTAG 524
Db         85 TGGTTTAAGTGGAAAGGGAATTACCACTAGATACTGGGATTGCTGCAAACCATCATGTGC 144

Qy        525 CTGGCCCGGTAAGGCCAA------TGTCAGTTCTCCTGTCAAGTCCTGTAACAAAGATGG 578
Db        145 TTGGGCAGACAATGTCAACACGCCTGATAAACAACCTCTTAAGTCGTGCAGAGTTGATGG 204

Qy        579 TGTCACTGCCCTTAGTGACAGCAATGTCCAAAGTGGCTGTAACGGTGGTAACAGTTACAT 638
Db        205 AGAAGCTGTAGCCCCACCTAATGATCCGTCTGGATGTGATATAAATGGTTCTTCGTTTGT 264

Qy        639 GTGTAACGACAACCAGCCTTGGGCTGTAAACGATAATCTTGCCTATGGTTTCGCTGCTGC 698
Db        265 ATGTAACAACAACCAACCGTATGTGGTTAACTCCACTTTATCCTATGGTTTTGCTTCTGC 324

Qy        699 TGCCATCAGTGGTGGTGGTGAATCTCGCTGGTGCTGTTCTTGTTTCGAACTTACTTTCAC 758
Db        325 TTCCTTTTCCGGTGGTATTGATACTAGCATGTGTTGTTCCTGCATGTTACTAAATTT--- 381

Qy        759 TTCTACCTCTGTTGCTGGTAAGAAGATGGTTATCCAAGTCACTAACACTGGTGGTGATCT 818
Db        382 TGAGGGTCAGCTGAAAGGAAAGCAATTCTTGGTTCAACTCACTAACTCTGGTGAAGAGTA 441

Qy        819 TGGCTCCTCTACTGGTGCTCACTTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTT 878
Db        442 TCAGACC---------AACCAATTTGATCTCGGTATCCCTGGAGGTGGAGTAGGTTTATT 492

Qy        879 ---CAATGGTTGCTCCAAGCAATGGGGTGCTCCCAATGACGGTTGGGGCTCGAGATACGG 935
Db        493 CCCCAAAGGGTGTACTGCTCAGTGGAACGCTCCCAGTACTGGTTGGGGTGACTTATACGG 552

Qy        936 TGGTATTTCTTCTGCATCTGACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTTGTAA 995
Db        553 AGGAGTCCATACTGAAGAAGAGTGTAACGAGCTTTCTGAAGTTTTACAACCAGGATGCAA 612

Qy        996 ATGGAGATTCA 1006
Db        613 ATGGAGGGTTA 623
```

RESULT 12
US-10-205-189A-244
; Sequence 244, Application US/10205189A
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Huesing, Joseph E.
; APPLICANT: Romano, Charles P.
; APPLICANT: Vetsch, Clayton S.
; APPLICANT: Hicks, Glenn R.
; TITLE OF INVENTION: Nucleic Acid Sequences from Diabrotica virgifera virgifera
; TITLE OF INVENTION: LeConte and Uses thereof
; FILE REFERENCE: 38-21(51497)C
; CURRENT APPLICATION NUMBER: US/10/205,189A
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/307,512
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9112
; SEQ ID NO 244
; LENGTH: 428
; TYPE: DNA
; ORGANISM: Diabrotica virgifera
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3026-001-Q1-E1-F4
US-10-205-189A-244

```
  Query Match             8.5%;  Score 94;  DB 8;  Length 428;
  Best Local Similarity   59.5%;  Pred. No. 1.4e-17;
  Matches  220;  Conservative    0;  Mismatches  135;  Indels   15;  Gaps    3;

Qy        722 CTCGCTGGTGCTGTTCTTGTTTCGAACTTACTTTCACTTCTACCTCTGTTGCTGGTAAGA 781
Db         17 CGCGTCCGTGTTGCGCTTGTTTCTTACTTAGCTTCAAAGAT---CAAATTTCAAACAAGA 73

Qy        782 AGATGGTTATCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCTACTGGTGCTCACT 841
Db         74 AAATGATTGTACAAGTTACAAATACTGGTTCTGAT---------TTGAGTCATAATCATT 124

Qy        842 TTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCA---ATGGTTGCTCCAAGCAAT 898
Db        125 TTGACATTGCTCTTCCCGGAGGTGGTGTTGGAATTTTCACACAAGGTTGTCATGACCAAT 184

Qy        899 GGGGTGCTCCCAATGACGGTTGGGGCTCGAGATACGGTGGTATTTCTTCTGCATCTGACT 958
Db        185 GGAATGCCCCATGGAACGGTTGGGGTGACCAATATGGTGGAGTTCATAACAGAGGCGAAT 244

Qy        959 GCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGA 1018
Db        245 GTGCTACTCTTCCTCAAGCGTTACAGTCTGGATGTTACTTTAGATTTGATTTCTACCAGA 304

Qy       1019 ACGCTGATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCCAAGGAAATCACCGCCA 1078
Db        305 ATGCTAACAATCCAAGAATGCATTTCGACCAAGTCCAATGCCCTGCTGAAATCGTTGCCA 364

Qy       1079 AGACAGGTTG 1088
Db        365 GATCTGGTTG 374
```

RESULT 13
US-10-205-189A-256
; Sequence 256, Application US/10205189A
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Huesing, Joseph E.
; APPLICANT: Romano, Charles P.
; APPLICANT: Vetsch, Clayton S.
; APPLICANT: Hicks, Glenn R.
; TITLE OF INVENTION: Nucleic Acid Sequences from Diabrotica virgifera virgifera
; TITLE OF INVENTION: LeConte and Uses thereof
; FILE REFERENCE: 38-21(51497)C
; CURRENT APPLICATION NUMBER: US/10/205,189A
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/307,512
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9112
; SEQ ID NO 256
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Diabrotica virgifera
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3026-011-Q1-E1-H7
US-10-205-189A-256

```
  Query Match             8.4%;  Score 92.4;  DB 8;  Length 416;
  Best Local Similarity   60.8%;  Pred. No. 4.3e-17;
  Matches  191;  Conservative    0;  Mismatches  111;  Indels   12;  Gaps    2;

Qy        778 AAGAAGATGGTTATCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCTACTGGTGCT 837
Db         43 AAGAAAATGATTGTACAAGTTACAAATACTGGTTCTGAT---------TTGAGTCATAAT 93

Qy        838 CACTTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCA---ATGGTTGCTCCAAG 894
Db         94 CATTTTGACATTGCTCTTCCCGGAGGTGGTGTTGGAATTTTCACACAAGGTTGTCATGAC 153

Qy        895 CAATGGGGTGCTCCCAATGACGGTTGGGGCTCGAGATACGGTGGTATTTCTTCTGCATCT 954
Db        154 CAATGGAATGCCCCATGGAACGGTTGGGGTGACCAATATGGTGGAGTTCATAACAGAGGC 213

Qy        955 GACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAACTGGTTC 1014
Db        214 GAATGTGCTACTCTTCCTCAAGCTTTACAGTCTGGATGTTACTTTAGATTTGATTTCTAC 273
```

```
Qy       1015 AAGAACGCTGATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCCAAGGAAATCACC 1074
Db        274 CAGAATGCTAACAATCCAAGAATGCATTTCGACCAAGTCCAATGCCCTGCTGAAATCGTT 333

Qy       1075 GCCAAGACAGGTTG 1088
Db        334 GCCAGATCTGGTTG 347


RESULT 14
US-10-205-189A-278
; Sequence 278, Application US/10205189A
; GENERAL INFORMATION:
;  APPLICANT: Andersen, Scott E.
;  APPLICANT:  Huesing, Joseph E.
;  APPLICANT:  Romano, Charles P.
;  APPLICANT:  Vetsch, Clayton S.
;  APPLICANT:  Hicks, Glenn R.
;  TITLE OF INVENTION: Nucleic Acid Sequences from Diabrotica virgifera virgifera
;  TITLE OF INVENTION:  LeConte and Uses thereof
;  FILE REFERENCE: 38-21(51497)C
;  CURRENT APPLICATION NUMBER: US/10/205,189A
;  CURRENT FILING DATE:  2002-07-24
;  PRIOR APPLICATION NUMBER: US 60/307,512
;  PRIOR FILING DATE: 2001-07-24
;  NUMBER OF SEQ ID NOS: 9112
; SEQ ID NO 278
;   LENGTH: 417
;   TYPE: DNA
;   ORGANISM: Diabrotica virgifera
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB3026-035-Q1-E1-G10
US-10-205-189A-278

  Query Match             8.2%;  Score 90.8;  DB 8;  Length 417;
  Best Local Similarity   60.5%;  Pred. No. 1.3e-16;
  Matches  190;  Conservative    0;  Mismatches  112;  Indels   12;  Gaps    2;

Qy        778 AAGAAGATGGTTATCCAAGTCACTAACACTGGTGGTGATCTTGGCTCCTCTACTGGTGCT 837
Db         17 AAGAAAATGATTGTACAAGTTACAAATACTGGTTCTGAT---------TTGAGTCATAAT 67

Qy        838 CACTTTGACTTGCAAATGCCCGGTGGTGGTGTTGGTATTTTCAAT---GGTTGCTCCAAG 894
Db         68 CATTTTGACATTGCTCTTCCCGGAGGTGGTGTTGGAATTTTCACTCAAGGTTGTCATGAC 127

Qy        895 CAATGGGGTGCTCCCAATGACGGTTGGGGCTCGAGATACGGTGGTATTTCTTCTGCATCT 954
Db        128 CAATGGAATGCCCCATGGAACGGTTGGGGTGACCAATATGGTGGAGTTCATAACAGAGGC 187

Qy        955 GACTGCTCTAGTCTTCCTTCCGCACTCCAAGCTGGTTGTAAATGGAGATTCAACTGGTTC 1014
Db        188 GAATGTGCTACCCTTCCTCAAGCTTTACAGTCTGGATGTTACTTTAGATTTGATTTCTAC 247

Qy       1015 AAGAACGCTGATAACCCAAGCATGACTTACAAGGAAGTTACCTGTCCCAAGGAAATCACC 1074
Db        248 CAGAATGCTAACAATCCAAGAATGCACTTCGACCAAGTCCAATGTCCTGCTGAAATCGTT 307

Qy       1075 GCCAAGACAGGTTG 1088
Db        308 GCCAGATCTGGTTG 321


RESULT 15
US-10-380-420-5
; Sequence 5, Application US/10380420
; GENERAL INFORMATION:
;  APPLICANT: Meiji Seika Kaisha, Ltd.
;  TITLE OF INVENTION: METHOD OF DEINKING WASTE PAPER USING CELLULASE WITHOUT LOWERING P
;  TITLE OF INVENTION:  STRENGTH AND EVALUATION METHOD THEREOF
;  FILE REFERENCE: VX032516 PCT
;  CURRENT APPLICATION NUMBER: US/10/380,420
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: PCT/JP01/08017
;  PRIOR FILING DATE: 2000-09-14
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Humicola insolens
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: (118)..(180)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (181)..()
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (178)..(452)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: Intron
;   LOCATION: (453)..(508)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (509)..(1088)
;   OTHER INFORMATION:
US-10-380-420-5

  Query Match             8.2%;  Score 89.8;  DB 8;  Length 1257;
  Best Local Similarity   58.9%;  Pred. No. 4.1e-16;
  Matches  201;  Conservative    0;  Mismatches  122;  Indels   18;  Gaps    2;

Qy        748 CTTACTTTCACTTCTACCTCTGTTGCTGGTAAGAAGATGGTTATCCAAGTCACTAACACT 807
Db        510 CTCACCTTCACATCCGGTCCTGTTGCTGGCAAGAAGATGGTCGTCCAGTCCACCAGCACT 569

Qy        808 GGTGGTGATCTTGGCTCCTCTACTGGTGCTCACTTTGACTTGCAAATGCCCGGTGGTGGT 867
Db        570 GGCGGTGATCTTGGCAGCAAC---------CACTTCGATCTCAACATCCCCGGCGGCGGC 620

Qy        868 GTTGGTATTTTCAATGGTTGCTCCAAGCAATGGGGTGCTCCCAATGACGGTTGGGGCTCG 927
Db        621 GTCGGCATCTTCGACGGATGCACTCCCCAGTTCGGCGGTC---------TGCCCGGCCAG 671

Qy        928 AGATACGGTGGTATTTCTTCTGCATCTGACTGCTCTAGTCTTCCTTCCGCACTCCAAGCT 987
Db        672 CGCTACGGCGGCATCTCGTCCCGCAACGAGTGCGATCGGTTCCCCGACGCCCTCAAGCCC 731

Qy        988 GGTTGTAAATGGAGATTCAACTGGTTCAAGAACGCTGATAACCCAAGCATGACTTACAAG 1047
Db        732 GGCTGCTACTGGCGCTTCGACTGGTTCAAGAACGCCGACAACCCGAGCTTCAGCTTCCGT 791

Qy       1048 GAAGTTACCTGTCCCAAGGAAATCACCGCCAAGACAGGTTG 1088
Db        792 CAGGTCCAATGCCCAGCCGAGCTCGTCGCTCGCACCGGATG 832


Search completed: June 18, 2003, 00:02:03
Job time : 806.766 secs
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